

CRF Errors Corrected by the STIC Systems Branch

0420 OIPE #8
7/25/2002

Serial Number: 097887,540A

CRF Processing Date: 7/25/2002
 Edited by: _____
 Verified by: AM (STIC sta)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**



OIPE

RAW SEQUENCE LISTING

DATE: 07/25/2002

PATENT APPLICATION: US/09/887,540A

TIME: 16:07:57

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\07252002\I887540A.raw

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4 <110> APPLICANT: Klein, Robert
6 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING LPR5 GENE
7   DISRUPTIONS
9 <130> FILE REFERENCE: R-193
11 <140> CURRENT APPLICATION NUMBER: US 09/887,540A
12 <141> CURRENT FILING DATE: 2001-06-21
14 <150> PRIOR APPLICATION NUMBER: US 60/213,201
15 <151> PRIOR FILING DATE: 2000-06-21
17 <150> PRIOR APPLICATION NUMBER: US 60/223,123
18 <151> PRIOR FILING DATE: 2000-08-07
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 5119
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
29 <400> SEQUENCE: 1
30 gccgcgcgcgc cgcaggcggg agcaagagcc gccgggagcc gcgaggatcc accgcgcgcg 60
31 cgcgcgcgccat ggagcccgag tgagcgcgcg gcgctcccgg ccgcccggacg acatggaaac 120
32 ggcgcgcgacc cgggccccctc cgcgcgcgcgc gccgcgcgctg ctgctgctgg tgctgtactg 180
33 cagcttggtc cccgcgcgcg cctcacgcgt cctgttggtt gccaacgcc gggatgtgcg 240
34 gctagtggat gccggcggag tgaagctgga gtccaccatt gtggccagtg gcctggagga 300
35 tgcagctgct gtagacttcc agttctccaa ggtgctgtg tactggacag atgtgagcga 360
36 ggaggccatc aaacagacct acctgaacca gactggagct gctgcacaga acattgtcat 420
37 ctgcggcctc gtgtcacctg atggcctggc ctgtgactgg gttggcaaga agctgtactg 480
38 gacggactcc gagaccaacc gcattgaggt tgccaacctc aatgggacgt cccgtaaggt 540
39 tctcttctg caggacctg accagccaag ggccattgcc ctggatcctg cacatgggta 600
40 catgtactgg actgactggg gggaagcacc ccgcatcgag cgggcagga tggatggcag 660
41 tacccggaag atcattgtag actccgacat ttactggccc aatgggctga ccatcgacct 720
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48 cactggtgtg cagttgcagg acaatggcaa gacgtgcaag acaggggctg aggaagtgtc 1140
49 gctgctggct cggaggacag acctgaggag gatctctctg gacaccctg acttcacaga 1200
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51 gggctacgtg tactggaccg atgatgaggt gcgggctatc cgcagggcgt acctagatgg 1320
52 ctgaggtgcg cagacacttg tgaacactga gatcaatgac cccgatggca ttgctgtgga 1380
53 ctgggtgcgc cggaacctct actggacaga tacaggcact gacagaattg aggtgactcg 1440
54 cctcaacggc acctcccgaa agatcctggt atctgaggac ctggacgaac cgcgagccat 1500
55 tgtgttgac cctgtgatgg gcctcatgta ctggacagac tggggggaga accccaaaat 1560

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57 gcccaatgga ctggccctgg acctgcagga gggcaagctg tactgggggg atgccaaaac 1680
58 tgataaaatc gaggtgatca acatagacgg gacaaagcgg aagaccctgc ttgaggacaa 1740
59 gctcccacac atttttgggt tcacactgct gggggacttc atctactgga ccgactggca 1800
60 gagacgcagt attgaaaggg tccacaaggt caaggccagc cgggatgtca tcattgatca 1860
61 actccccgac ctgatgggac tcaaagccgt gaatgtggcc aaggttgtcg gaaccaaccc 1920
62 atgtgcggat ggaaatggag ggtgcagcca tctgtgcttc ttcacccac gtgccaccaa 1980
63 gtgtggctgc cccattggcc tggagctgtt gagtgcacatg aagacctgca taatccccga 2040
64 ggccctcctg gtattcacca gcagagccac catccacagg atctccctgg agactaacia 2100
65 caacgatgtg gctatccac tcacgggtgt caaagaggcc tctgcactgg actttgatgt 2160
66 gtccaacaat cacatctact ggactgatgt tagcctcaag acgatcagcc gagccttcat 2220
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69 ggcccggctg gatgggcagt tccggcaggt gcttgtgtgg agagaccttg acaaccccag 2400
70 gtctctggct ctggatccta ctaaaggcta catctactgg actgagtggg gtggcaagcc 2460
71 aaggattgtg cgggccttca tggatgggac caattgtatg acactggtag acaaggtggg 2520
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87 ggtcctcttc accacaggcc tcatccgtcc cgtggccctt gtggtggaca atgctctggg 3480
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92 ggaggaagtc agcctggagg agttctcagc ccatcctgtg gcccgagaca atggcggctg 3780
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99 cagcggccag tgtgtcctca tcaagcaaca gtgtgactcc tccccgact gtgctgatg 4200
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102 ctttgtctgc cagcgtgtga tgtgccagcg ctacacagg gccagtgggc ctttcccca 4380
103 cgagtatgtt ggtggagccc ctcatgtgcc tctcaacttc atagccccag gtggctcaca 4440
104 gcacggctcc tcccaggca tcccgtcag caagtccgtg atgagctcca tgagcctggt 4500

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105 ggggggggcgc ggcagcgtgc ccctctatga ccggaatcac gtcactgggg cctcatccag 4560
106 cagctcgtcc agcacaaagg ccacactata tccgccgata ctgaacccac ccccgcccc 4620
107 ggccacagac ccctctctct acaacgtgga cgtgttttat tcttcaggca tcccggccac 4680
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109 cacagatgtg tgtgacagtg actacagcat cagtcgctgg aagagcagca aatactacct 4800
110 ggacttgaat tcggactcag acccctaccc ccccccggcc acccccacac gccagtaoct 4860
111 atctgcagag gacagctgcc caccctcacc aggcactgag aggagtact gccacctott 4920
112 cccgccccca cgtccccct gcacggactc gtcctgacct cggccgtcca cccggccctg 4980
113 ctgcctccct gtaaatatgt ttaaatatga acaaaggaaa aatatatgtt atgatttaaa 5040
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115 ggctgggaaa cttttctag                                     5119
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118 <211> LENGTH: 1614
119 <212> TYPE: PRT
120 <213> ORGANISM: Mus musculus
122 <400> SEQUENCE: 2
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124 1 5 10 15
125 Leu Leu Leu Val Leu Tyr Cys Ser Leu Val Pro Ala Ala Ala Ser Pro
126 20 25 30
127 Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala Gly
128 35 40 45
129 Gly Val Lys Leu Glu Ser Thr Ile Val Ala Ser Gly Leu Glu Asp Ala
130 50 55 60
131 Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr Asp
132 65 70 75 80
133 Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly Ala
134 85 90 95
135 Ala Ala Gln Asn Ile Val Ile Ser Gly Leu Val Ser Pro Asp Gly Leu
136 100 105 110
137 Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu Thr
138 115 120 125
139 Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val Leu
140 130 135 140
141 Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala Leu Asp Pro Ala
142 145 150 155 160
143 His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Ala Pro Arg Ile Glu
144 165 170 175
145 Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser Asp
146 180 185 190
147 Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys Leu
148 195 200 205
149 Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu Asp
150 210 215 220
151 Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro Phe
152 225 230 235 240
153 Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln Thr
154 245 250 255
155 Arg Ser Ile His Ala Cys Asn Lys Trp Thr Gly Glu Gln Arg Lys Glu

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156		260		265		270
157	Ile	Leu	Ser	Ala	Leu	Tyr
158						
159	Glu	Arg	Gln	Pro	Pro	Phe
160						
161	Cys	Ser	His	Leu	Cys	Leu
162						
163	Ala	Cys	Pro	Thr	Gly	Val
164						
165	Thr	Gly	Ala	Glu	Glu	Val
166						
167	Arg	Ile	Ser	Leu	Asp	Thr
168						
169	Gly	Asp	Ile	Arg	His	Ala
170						
171	Tyr	Val	Tyr	Trp	Thr	Asp
172						
173	Leu	Asp	Gly	Ser	Gly	Ala
174						
175	Pro	Asp	Gly	Ile	Ala	Val
176						
177	Asp	Thr	Gly	Thr	Asp	Arg
178						
179	Arg	Lys	Ile	Leu	Val	Ser
180						
181	Leu	His	Pro	Val	Met	Gly
182						
183	Pro	Lys	Ile	Glu	Cys	Ala
184						
185	Val	Asn	Thr	Ser	Leu	Gly
186						
187	Glu	Gly	Lys	Leu	Tyr	Trp
188						
189	Ile	Asn	Ile	Asp	Gly	Thr
190						
191	Pro	His	Ile	Phe	Gly	Phe
192						
193	Asp	Trp	Gln	Arg	Arg	Ser
194						
195	Arg	Asp	Val	Ile	Ile	Asp
196						
197	Val	Asn	Val	Ala	Lys	Val
198						
199	Gly	Gly	Cys	Ser	His	Leu
200						
201	Gly	Cys	Pro	Ile	Gly	Leu
202						
203	Ile	Pro	Glu	Ala	Phe	Leu
204						

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205 Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile Pro Leu Thr Gly
206          660          665          670
207 Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His Ile
208          675          680          685
209 Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg Ala Phe Met Asn
210          690          695          700
211 Gly Ser Ser Val Glu His Val Ile Glu Phe Gly Leu Asp Tyr Pro Glu
212 705          710          715          720
213 Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp Thr
214          725          730          735
215 Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg Gln
216          740          745          750
217 Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu Asp
218          755          760          765
219 Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro Arg
220          770          775          780
221 Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val Asp
222 785          790          795          800
223 Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln Arg
224          805          810          815
225 Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn Met
226          820          825          830
227 Leu Gly Gln Glu Arg Met Val Ile Ala Asp Asp Leu Pro Tyr Pro Phe
228          835          840          845
229 Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn Leu
230          850          855          860
231 His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr Leu
232 865          870          875          880
233 Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His Ser
234          885          890          895
235 Ser Arg Gln Asp Gly Leu Asn Asp Cys Val His Ser Asn Gly Gln Cys
236          900          905          910
237 Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys Ala
238          915          920          925
239 Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro Ser
240          930          935          940
241 Thr Phe Leu Leu Phe Ser Gln Lys Phe Ala Ile Ser Arg Met Ile Pro
242 945          950          955          960
243 Asp Asp Gln Leu Ser Pro Asp Leu Val Leu Pro Leu His Gly Leu Arg
244          965          970          975
245 Asn Val Lys Ala Ile Asn Tyr Asp Pro Leu Asp Lys Phe Ile Tyr Trp
246          980          985          990
247 Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr Gln
248          995          1000          1005
249 Pro Ser Met Leu Thr Ser Pro Ser Gln Ser Leu Ser Pro Asp Arg Gln
250          1010          1015          1020
251 Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp Thr
252 1025          1030          1035          1040
253 Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu Asp Gly Asp Ala

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VERIFICATION SUMMARY

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